In this issue of *Transcription*

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TFIIF and Transcript Initiation pp. 156–159

The general transcription factor TFIIF is essential for assembly of RNAP II preinitiation complexes on fully double-stranded templates *in vitro*. Although existing models assign various tasks to TFIIF during preinitiation complex formation and transcript initiation, recent results suggest that some aspects of those models may need to be revised. In this issue of *Transcription*, Luse discusses recently published manuscripts that emphasize the significance of the interaction of TFIIF and TFIIB and raise the possibility that a fraction of RNAP II transcription complex assembly proceeds through a pathway that is independent of TFIIF.

σ 70 and PhoB Get a Better Grip pp. 160–164

Canals et al. discuss the recently obtained crystal structure of a bacterial transcription subcomplex comprising the effector domain of factor PhoB, its target DNA and the σ 4 domain of the RNA polymerase σ 70 subunit. This structure supports the notion that a stronger grip on the promoter-factor complex results in an enhanced RNAP architecture.

Endocrine Resistance in Breast Cancer: Epigenetic Mechanisms pp. 165–170

The genomics events promoting the dysregulation of gene expression during endocrine resistance in breast cancer are

not clearly understood. Multiple cellular mechanisms have been proposed to be involved. Now, Bianco and Gvry review the signaling pathways involved in endocrine resistance in the context of recent epigenetic studies.

On How Enhancers Work pp. 181–186

Enhancers are often located at large distances from gene promoters within the non-coding genome. Stadhouders et al. propose that enhancers not only can stimulate transcription initiation by communicating with promoters via chromatin looping mechanisms but may also stimulate transcription elongation by physical interactions with intronic elements. The authors review recent findings from studies of the hematopoietic system.

HCF-1 and Cell Cycle Regulation pp. 187–192

Initially discovered as a cofactor in multiprotein DNA complexes that form on Herpes Simplex Virus immediate early gene promoters to activate the transcription of viral genes, HCF-1 is an abundant chromatin-associated protein that also regulates various stages of the cell cycle. Recently, HCF-1 was shown to interact with diverse E2F proteins to induce cell cycle-specific transcription. In this issue of *Transcription*, Zargar and Tyagi review the diversity of HCF-E2F interactions and the variety of multiprotein complexes it occurs in, to influence the local chromatin landscape at E2F-promoters.

Transcription at Centromeres in Budding Yeast pp. 193–197

Centromeres are specialized chromosomal loci that are essential for proper chromosome segregation. Recent data show that a certain level of active transcription, regulated by transcription factors Cbf1 and Ste12, makes a direct contribution to centromere function in budding yeast. Ohkuni and Kitagawa now discuss the requirement and function of transcription at centromeres.

Terminating Transcription Between Closely Spaced Genes pp. 198–212

In this issue of *Transcription*, Henriques et al. study transcription termination between closely spaced genes of *Drosophila*, where about 52% of tandem genes are separated by regions of less than 1 kb. The authors show that an intergenic spacing of 168 bp is sufficient for efficient transcription termination between the *polo-snap* tandem gene pair. For the *polo-snap* pair, displacement of the poised polymerase from the *snap* promoter by depletion of the initiation factor TFIIB results in an increase of *polo* transcriptional read-through, which suggests that poised polymerase is necessary for transcription termination. Interestingly, the authors show that *polo* forms a TFIIB dependent gene loop between its promoter and terminator regions. In addition, deletion of the *polo* promoter causes an increase in *snap* expression, as does deletion of *polo* poly(A) signals.